

SEQUENCE LISTING

<110> Sheppard, Paul O.
Gilbertson, Debra G.

<120> SECRETED PROTEINS ENCODED BY HUMAN CHROMOSOME 13

<130> 97-38C1

<150> 60/053,613

<151> 1997-07-24

<150> 09/122,383

<151> 1998-07-24

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<212> DNA

<213> Homo sapien

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<221> CDS

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Gly Ala Gly Ala Ala Arg Gly Arg Ala Ser Trp Cys Trp Ala Leu Ala	
5 10 15	

ctg ctt tgg ctc gcg gtg gtt ccg ggc tgg tcc cgg gtc tcg ggc atc	151
Leu Leu Trp Leu Ala Val Val Pro Gly Trp Ser Arg Val Ser Gly Ile	
20 25 30 35	

ccc tcc cgg cgc cac tgg ccg gtg ccc tac aag cgc ttt gac ttc cgt	199
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Pro	Ser	Arg	Arg	His	Trp	Pro	Val	Pro	Tyr	Lys	Arg	Phe	Asp	Phe	Arg	
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cca	aaa	cct	gat	cct	tat	tgt	caa	gct	aag	tat	act	ttc	tgt	cca	act	247
Pro	Lys	Pro	Asp	Pro	Tyr	Cys	Gln	Ala	Lys	Tyr	Thr	Phe	Cys	Pro	Thr	
			55					60					65			
ggc	tca	cct	atc	cca	gtt	atg	gag	ggc	gat	gat	gac	att	gaa	gtt	ttt	295
Gly	Ser	Pro	Ile	Pro	Val	Met	Glu	Gly	Asp	Asp	Asp	Ile	Glu	Val	Phe	
		70					75					80				
cga	tta	caa	gcc	cca	gta	tgg	gaa	ttt	aaa	tat	gga	gac	ctc	ctg	gga	343
Arg	Leu	Gln	Ala	Pro	Val	Trp	Glu	Phe	Lys	Tyr	Gly	Asp	Leu	Leu	Gly	
	85					90					95					
cac	ttg	aaa	att	atg	cat	gat	gcc	att	gga	ttc	aga	agt	aca	tta	act	391
His	Leu	Lys	Ile	Met	His	Asp	Ala	Ile	Gly	Phe	Arg	Ser	Thr	Leu	Thr	
100					105				110						115	
ggc	aag	aac	tac	aca	atg	gaa	tgg	tat	gaa	ctt	ttc	caa	ctt	ggc	aac	439
Gly	Lys	Asn	Tyr	Thr	Met	Glu	Trp	Tyr	Glu	Leu	Phe	Gln	Leu	Gly	Asn	
				120					125					130		
tgt	aca	ttt	ccc	cat	ctc	cga	cct	gaa	atg	gat	gcc	cct	ttc	tgg	tgt	487
Cys	Thr	Phe	Pro	His	Leu	Arg	Pro	Glu	Met	Asp	Ala	Pro	Phe	Trp	Cys	
			135					140					145			
aat	caa	ggc	gct	gcc	tgc	ttt	ttt	gag	gga	att	gat	gat	gtt	cac	tgg	535
Asn	Gln	Gly	Ala	Ala	Cys	Phe	Phe	Glu	Gly	Ile	Asp	Asp	Val	His	Trp	
		150					155					160				
aag	gaa	aat	ggg	aca	tta	gtt	caa	gta	gca	act	ata	tca	gga	aac	atg	583
Lys	Glu	Asn	Gly	Thr	Leu	Val	Gln	Val	Ala	Thr	Ile	Ser	Gly	Asn	Met	
	165					170					175					
ttc	aac	caa	atg	gca	aag	tgg	gtg	aaa	cag	gac	aat	gaa	aca	gga	att	631
Phe	Asn	Gln	Met	Ala	Lys	Trp	Val	Lys	Gln	Asp	Asn	Glu	Thr	Gly	Ile	
180					185					190					195	
tat	tat	gag	aca	tgg	aat	gta	aaa	gcc	agc	cca	gaa	aag	ggg	gca	gag	679
Tyr	Tyr	Glu	Thr	Trp	Asn	Val	Lys	Ala	Ser	Pro	Glu	Lys	Gly	Ala	Glu	
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 Thr Trp Phe Asp Ser Tyr Asp Cys Ser Lys Phe Val Leu Arg Thr Phe
 215 220 225

aac aag ttg gct gaa ttt gga gca gag ttc aag aac ata gaa acc aac 775
 Asn Lys Leu Ala Glu Phe Gly Ala Glu Phe Lys Asn Ile Glu Thr Asn
 230 235 240

tat aca aga ata ttt ctt tac agt gga gaa cct act tat ctg gga aat 823
 Tyr Thr Arg Ile Phe Leu Tyr Ser Gly Glu Pro Thr Tyr Leu Gly Asn
 245 250 255

gaa aca tct gtt ttt ggg cca aca gga aac aag act ctt ggt tta gcc 871
 Glu Thr Ser Val Phe Gly Pro Thr Gly Asn Lys Thr Leu Gly Leu Ala
 260 265 270 275

ata aaa aga ttt tat tac ccc ttc aaa cca cat ttg cca act aaa gaa 919
 Ile Lys Arg Phe Tyr Tyr Pro Phe Lys Pro His Leu Pro Thr Lys Glu
 280 285 290

ttt ctg ttg agt ctc ttg caa att ttt gat gca gtg att gtg cac aaa 967
 Phe Leu Leu Ser Leu Leu Gln Ile Phe Asp Ala Val Ile Val His Lys
 295 300 305

cag ttc tat ttg ttt tat aat ttt gaa tat tgg ttt tta cct atg aaa 1015
 Gln Phe Tyr Leu Phe Tyr Asn Phe Glu Tyr Trp Phe Leu Pro Met Lys
 310 315 320

ttc cct ttt att aaa ata aca tat gaa gaa atc cct tta cct atc aga 1063
 Phe Pro Phe Ile Lys Ile Thr Tyr Glu Glu Ile Pro Leu Pro Ile Arg
 325 330 335

aac aaa aca ctc tct ggt tta taaaacacct taattctact gctctttttt 1114
 Asn Lys Thr Leu Ser Gly Leu
 340 345

tctccaatca ccagcatctg tttttcaggg ggtgatttta cttttgtgaa ttccttagcc 1174
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 <213> Homo sapien

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Ser	Gly	Ile	Pro	Ser	Arg	Arg	His	Trp	Pro	Val	Pro	Tyr	Lys	Arg	Phe	35	40	45	
Asp	Phe	Arg	Pro	Lys	Pro	Asp	Pro	Tyr	Cys	Gln	Ala	Lys	Tyr	Thr	Phe	50	55	60	
Cys	Pro	Thr	Gly	Ser	Pro	Ile	Pro	Val	Met	Glu	Gly	Asp	Asp	Asp	Ile	65	70	75	80
Glu	Val	Phe	Arg	Leu	Gln	Ala	Pro	Val	Trp	Glu	Phe	Lys	Tyr	Gly	Asp	85	90	95	
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Thr	Leu	Thr	Gly	Lys	Asn	Tyr	Thr	Met	Glu	Trp	Tyr	Glu	Leu	Phe	Gln	115	120	125	
Leu	Gly	Asn	Cys	Thr	Phe	Pro	His	Leu	Arg	Pro	Glu	Met	Asp	Ala	Pro	130	135	140	
Phe	Trp	Cys	Asn	Gln	Gly	Ala	Ala	Cys	Phe	Phe	Glu	Gly	Ile	Asp	Asp	145	150	155	160
Val	His	Trp	Lys	Glu	Asn	Gly	Thr	Leu	Val	Gln	Val	Ala	Thr	Ile	Ser	165	170	175	
Gly	Asn	Met	Phe	Asn	Gln	Met	Ala	Lys	Trp	Val	Lys	Gln	Asp	Asn	Glu	180	185	190	
Thr	Gly	Ile	Tyr	Tyr	Glu	Thr	Trp	Asn	Val	Lys	Ala	Ser	Pro	Glu	Lys	195	200	205	
Gly	Ala	Glu	Thr	Trp	Phe	Asp	Ser	Tyr	Asp	Cys	Ser	Lys	Phe	Val	Leu	210	215	220	
Arg	Thr	Phe	Asn	Lys	Leu	Ala	Glu	Phe	Gly	Ala	Glu	Phe	Lys	Asn	Ile	225	230	235	240
Glu	Thr	Asn	Tyr	Thr	Arg	Ile	Phe	Leu	Tyr	Ser	Gly	Glu	Pro	Thr	Tyr	245	250	255	
Leu	Gly	Asn	Glu	Thr	Ser	Val	Phe	Gly	Pro	Thr	Gly	Asn	Lys	Thr	Leu	260	265	270	
Gly	Leu	Ala	Ile	Lys	Arg	Phe	Tyr	Tyr	Pro	Phe	Lys	Pro	His	Leu	Pro	275	280	285	

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Thr Lys Glu Phe Leu Leu Ser Leu Leu Gln Ile Phe Asp Ala Val Ile
 290 295 300
 Val His Lys Gln Phe Tyr Leu Phe Tyr Asn Phe Glu Tyr Trp Phe Leu
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 Pro Met Lys Phe Pro Phe Ile Lys Ile Thr Tyr Glu Glu Ile Pro Leu
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 Pro Ile Arg Asn Lys Thr Leu Ser Gly Leu
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tggccngtnc	cntayaarmg	nttygaytty	mgncnaarc	cngayccnta	ytgycargcn	180
aartayacnt	tytgyccnac	nggnwsnccn	athccngtna	tggarggnga	ygaygayath	240
gargtnttym	gnytncargc	nccngtntgg	garttyaart	ayggngayyt	nytnggnca	300
ytnaaratha	tgcaygaygc	nathggntty	mgwnsnacny	tnacnggnaa	raaytayacn	360
atggartggt	aygarynttt	ycarytnggn	aaytgyacnt	tyccncayyt	nmgnccngar	420
atggaygcnc	cnttytggtg	yaaycarggn	gcngcntgyt	tyttygargg	nathgaygay	480
gtncaytgga	argaraaygg	nacnytngtn	cargtngcna	cnathwsngg	naayatgtty	540
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aaygtnaarg	cnwsnccnga	raarggngcn	garacntggt	tygaywsnta	ygaytgywsn	660
aarttygtny	tnmgnaacntt	yaayaarytn	gcngarttyg	gngcngartt	yaaraayath	720
garacnaayt	ayacnmgnat	httyyntay	wsngngarc	cnacntayyt	nggnaaygar	780
acnwsngtnt	tyggncnac	nggnaayaar	acnytnggny	tngcnathaa	rmgnttytay	840
tayccnttya	arccncayyt	nccnacnaar	garttyytny	tnwsnytnyt	ncarathtty	900
gaygcngtna	thgtncayaa	rcarttytay	ytnttytaya	ayttygarta	ytggttyytn	960
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<223> Glu-Glu affinity tag peptide

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